

Table S2. The top 10 enriched process networks from *MetaCore* for functional annotation of 217 candidate target genes.

#	Significant process networks	Total genes	In our data	p-value
1	Cell adhesion_Synaptic contact	184	13	1.467×10^{-4}
2	Development_Neurogenesis in general	192	12	8.064×10^{-4}
3	Development_Hedgehog signaling	254	14	1.038×10^{-3}
4	Signal transduction_WNT signaling	177	11	1.394×10^{-3}
5	Signal Transduction_TGF-beta, GDF and Activin signaling	154	10	1.654×10^{-3}
6	Cell adhesion_Attractive and repulsive receptors	175	10	4.204×10^{-3}
7	Reproduction_FSH-beta signaling pathway	160	9	7.211×10^{-3}
8	Development_Regulation of angiogenesis	223	11	8.168×10^{-3}
9	Cardiac development_BMP_TGF_beta_signaling	117	7	1.252×10^{-2}
10	Neurophysiological process_Melatonin signaling	43	4	1.304×10^{-2}